

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:46:14 ; Search time 35.44 Seconds

(without alignments)  
75.917 Million cell updates/sec

Title: US-09-785-059-1

Perfect score: 135

Sequence: 1 RVIRVORACRAIRHIVRIROGLRIL 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	83.0	861	1 VCLJLV	env polypotein pr
2	102	75.6	357	2 S21990	env polypotein pr
3	102	75.6	846	1 VCLJND	env polypotein pr
4	101	74.8	851	2 S33985	env polypotein pr
5	101	74.8	856	1 VCLJH3	env polypotein pr
6	101	74.8	856	1 VCLJVL	env polypotein pr
7	101	74.8	856	1 VCLJ3W	env polypotein pr
8	99	73.3	854	2 S13288	env polypotein pr
9	98	72.6	358	2 S22002	env polypotein pr
10	98	72.6	853	2 S54384	env polypotein pr
11	97	71.9	358	2 S22000	env polypotein pr
12	97	71.9	358	2 S70417	env polypotein pr
13	97	71.9	852	2 T12016	env polypotein pr
14	94	69.6	357	2 S22006	env polypotein pr
15	94	69.6	855	1 VCLJAJ2	env polypotein pr
16	92	68.1	852	1 VCLJBR	env polypotein pr
17	90	66.7	357	2 S21994	env polypotein pr
18	86	63.7	357	2 S22004	env polypotein pr
19	86	63.7	859	1 VCLJMN	env polypotein pr
20	85	63.0	358	2 S21998	env polypotein pr
21	84	62.2	856	1 A44963	env polypotein pr
22	84	62.2	861	1 VCLJSC	env polypotein pr
23	83	61.5	843	1 H44001	env polypotein pr
24	83	61.5	868	1 VCLJH4	env polypotein pr
25	82	60.7	357	2 S21996	env polypotein pr
26	82	60.7	357	2 S21992	env polypotein pr
27	78	57.8	847	2 T09448	env polypotein pr
28	78	57.8	847	2 S13289	env polypotein pr
29	77	57.0	859	2 T01672	env polypotein pr

30	77	57.0	861	1 VCLJKB	env polypotein pr
31	75	55.6	855	1 VCLJZR	env polypotein pr
32	70	51.9	854	1 VCLJSI	env polypotein pr
33	64	47.4	863	2 A53034	env polypotein pr
34	58	43.0	877	2 S45197	env polypotein pr
35	56	41.5	859	2 S24571	env polypotein pr
36	54.5	40.4	864	1 VCLJG4	env polypotein pr
37	49.5	36.7	153	2 F86331	env polypotein pr
38	49	36.3	855	2 A45713	env polypotein pr
39	49	36.3	858	2 VCLJG2	env polypotein pr
40	48.5	35.9	1571	2 T13711	env polypotein pr
41	48	35.6	420	2 AB0098	env polypotein pr
42	48	35.6	456	2 C82785	env polypotein pr
43	48	35.6	877	2 C46356	env polypotein pr
44	47.5	35.2	268	2 AF2470	env polypotein pr
45	47	34.8	101	2 S22454	env polypotein pr

## ALIGNMENTS

RESULT 1  
VCLJLV  
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Main-Hodson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85099333  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAT>  
A:Cross-references: GB:K02013; NID:q326417; PIDN:AAB59751.1; PID:q326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,337,344,361,391,397,402,  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status pre  
Query Match 83.0%; Score 112; DB 1; Length 861;  
Best Local Similarity 85.7%; Pred. No. 1e-07;  
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 RVIRVORACRAIRHIVRIROGLRIL 28  
DB 833 RVIEVVGACRAIRHIVRIROGLRIL 860  
RESULT 2  
S21990  
env polypotein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 20  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21990; S70423  
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL data library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21990  
A:Molecule type: DNA  
A:Residues: 1-357 <STEL>  
A:Cross-references: EMBL:X61357; NID:q60175; PIDN:CAA43626.1; PID:q60176  
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MID:92244209

A:Accession: S70423

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332, 'X', 334-357 <STE2>

A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176

C:Superfamily: type E retrovirus env polyprotein

#### Query Match

Best Local Similarity 75.6%; Score 102; DB 2; Length 357;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 RVIRVORACRAIRHVRIRIROGLRRL 28

DB 329 RVIEVORACRAIRHVRIRIROGLRRL 356

#### RESULT 3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: J00066

R:Splice, B.: Site, J.: Zachar, V.: Rey, F.: Barre-Sinoussi, F.: Galibert, F.: Hampe, A.:

Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus

A:Reference number: J00065; MID:90034200

A:Accession: J00066

A:Molecule type: DNA

A:Residues: 1-846 <SPI>

A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162

A:Note: the authors translated the codon GCG for residue 523 as Arg

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-501/Product: coat protein gp120 #status predicted <CP1>

F:502-846/Product: coat protein gp41 #status predicted <CP2>

F:502-520/Domain: transmembrane #status predicted <TM>

F:574-692/Domain: transmembrane #status predicted <TM2>

F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

#### Query Match

Best Local Similarity 75.6%; Score 102; DB 1; Length 846;

Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 RVIRVORACRAIRHVRIRIROGLRRL 28

DB 818 RVIEVORACRAIRHVRIRIROGLRRL 845

#### RESULT 4

env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:960199

C:Superfamily: type E retrovirus env polyprotein

#### Query Match

Best Local Similarity 74.8%; Score 101; DB 2; Length 851;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 RVIRVORACRAIRHVRIRIROGLRRL 28

DB 823 RVIEVORACRAIRHVRIRIROGLRRL 850

#### RESULT 5

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; D

enberg, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; MID:85111123

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>

A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F:512-856/Product: transmembrane glycoprotein #status predicted <TM>

F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,

F:511,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

#### Query Match

Best Local Similarity 74.8%; Score 101; DB 1; Length 856;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 RVIRVORACRAIRHVRIRIROGLRRL 28

DB 828 RVIEVORACRAIRHVRIRIROGLRRL 855

#### RESULT 6

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03974

R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J

Nature 313, 450-458, 1985

A:Title: Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retr

A:Reference number: A93355; MID:85111157

A:Accession: A03974

A:Molecule type: DNA

A:Residues: 1-856 <MUE>

A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:9328559

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>

F:512-856/Product: transmembrane glycoprotein #status predicted <TM>

F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,



A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351  
C:Superfamily: type E retrovirus env polyprotein

Query Match	71.9%;	Score 97;	DB 2;	Length 358;
Best Local Similarity	75.0%;	Pred. No. 5.7e-06;		
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Qy	1	RVIRVQACRAIRHIVRIRQGLRRL	28
Db	330	RVLEVXQRCRAIRLHPRIRQGLERSL	357

RESULT 12  
S70417  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)  
C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
C:Accession: S70417  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MID:92144209

A:Accession: S/041/  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-358 <STE>  
A:Cross-references: EMBL:X61351; NID:g60184; PID:CAA43614.1; PID:g60185  
C:Superfamily: type E retrovirus env polypotein

Query Match	71.9%;	Score 97;	DB 2;	Length 358;
Best Local Similarity	75.0%;	Pred. No. 5.7e-06;		
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

Oy            1 RVIRVQACRAIRHIVRIRQGLRIL 28  
               ||| | | | | | | | |  
Db           330 RVEIEXQRXCRAILHIPRIQGLERSL 357

RESULT 13  
T12016  
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C.Accession: T12016  
R.McCutchan, F.E.: Sanders-Buell, E.: Salminen, M.O.: Carr, J.K.: Sheppard, W.H  
Aids Res. Hum. Retroviruses 14, 329-337, 1998

A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in  
A:Reference number: Z17379; MUID:98178716  
A:Accession: 112016

```

n,status: preliminary, translated from gb/emb/emb
A;molecule type: DNA
A;Residues: 1-852 <MCC>

```

C1:cross\_references: EMBL:030534, NID:9422100, FID:9422111, FID:9422112  
 C1:genetics:  
 A1:gene: env  
 C1:superfamily: type E retrovirus env polypotein

Query Match	71.9%	Score 911	DB 2	Length 852
Best Local Similarity	75.0%	Pred. No. 1.2e-05		
Matches	21	Conservative	0	Mismatches 7
				Indels 0
				Gaps 0

QY 1 RVRVQGRACRAIRHVRIRIQGLRRIL 28  
||| ||| ||| ||| ||| ||| |||  
Db 824 WIEWQRTCRALHIPTRIQGLERAL 85

RESULT 14  
S22006  
antigen specific human immunodeficiency virus type 1 (patient 41)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1995  
C:Accession: S70420; S22006  
R:Steuiler, H.; Storch-Hagenlocher, B.; Wildemann, B.

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID: 92144209  
A:Accession: S70420

A:Residues: 1-357 <ST2>  
A:Molecule type: DNA  
A:Category: FcRANKL

A:Cross-references: EMBL:X61354; NID:g60190; PIDN:CA43620.1; PID:g6019  
A:Experimental source: patient L  
A:Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polypepten

Query Match	69.6%;	Score 94;	DB 2;	Length 357;
Best Local Similarity	-71.4%;	Pred. No. 1.5e-05;		
Matches	20;	Conservative	2;	Mismatches 6;
				Indels 0;
				Gaps 0.

```
QY      1 RVIRVQACRAIRHIVRRIRQGLRRL 28
      ||| ::||| ||| ||| ||| ||| |||
Db      329 RVIEITQRAYRAILHPIPRIRQGLERAL 356
```

RESULT 15  
VCLJA2  
env polypeptin precursor - human immunodeficiency virus type 1 (isolate ARV-2,  
N:Alternate names: coat polypeptin

C:Accession: A03976  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

A>Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)  
A1:JOURNAL: FEBS LETTERS  
A2:1985  
A3:227, 484-492, 1985

A/Accession: A03570  
A/Molecule type: DNA  
A/Residues: 1-855 <SAN>

C;Genetics :  
A;Gene: env  
C : Superfamily: type E retrovirus env pol/protein

C;isopermethrinyl type A bicyclic compound  
C;Keratoins: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly-  
F;1-30/Domains: signal sequence #status predicted <STG>  
F;31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;817-885/Product: transmembrane glycoprotein #status predicted <TM>  
E;878,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445  
F;610,624,636,615/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match	69.68;	Score 94;	DB 1;	Length 855;
Best Local Similarity	75.08;	Pred. No. 3.1e-05;		
Matches	21;	Conservative	1;	Mismatches 6;
			Indels	0;
			Gaps	0

```

QY      1 RVIRVQACRAIRHIVRIRQGLRIL 28
      ||| | ||| ||| | ||| ||| | :|
Db      827 RVIEVAQRAYRAILHHRIRQGLERLL 854

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Search completed: August 14, 2002, 10:51:20  
Job time: 306 sec